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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/194,552DATE: 04/19/2000
TIME: 10:19:36

Input Set: I194552.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

p# //

1 <110> APPLICANT: Brooks, Peter
2 Cheresh, David A.
3 Friedlander, Martin
4 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
5 ALPHAVBETA5 MEDIATED ANGIOGENESIS
6 <130> FILE REFERENCE: MER0065S
7 <140> CURRENT APPLICATION NUMBER: US/09/194,552
8 <141> CURRENT FILING DATE: 1999-03-23
9 <150> EARLIER APPLICATION NUMBER: PCT/US97/09099
10 <151> EARLIER FILING DATE: 1997-05-30
11 <150> EARLIER APPLICATION NUMBER: 60/018,773
12 <151> EARLIER FILING DATE: 1996-05-31
13 <150> EARLIER APPLICATION NUMBER: 60/015,869
14 <151> EARLIER FILING DATE: 1996-05-31
15 <160> NUMBER OF SEQ ID NOS: 43
16 <170> SOFTWARE: PatentIn Ver. 2.0
17 <210> SEQ ID NO 1
18 <211> LENGTH: 5
19 <212> TYPE: PRT
20 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
23 <220> FEATURE:
24 <221> NAME/KEY: PEPTIDE
25 <222> LOCATION: (1)..(5)
26 <223> OTHER INFORMATION: BOC signifies the N-terminal protecting group
27 butyloxycarbonyl; OMe signifies a C-terminal
28 methyl ester; arginine in the first position.
29 <220> FEATURE:
30 <221> NAME/KEY: PEPTIDE
31 <222> LOCATION: (1)..(5)
32 <223> OTHER INFORMATION: OMe signifies the C-terminal protecting group
33 methyl ester.
34 <220> FEATURE:
35 <221> NAME/KEY: PEPTIDE
36 <222> LOCATION: (1)..(5)
37 <223> OTHER INFORMATION: A prefix "D" in D-phe signifies that the
38 phenylalanine in position 4 is a D-amino acid.
39 <400> SEQUENCE: 1
40 Arg Gly Asp Phe Val
41 1 5
42 <210> SEQ ID NO 2
43 <211> LENGTH: 5
44 <212> TYPE: PRT

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45 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
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48 <220> FEATURE:
49 <221> NAME/KEY: PEPTIDE
50 <222> LOCATION: (1)..(5)
51 <223> OTHER INFORMATION: BOC signifies the N-terminal blocking group
52 tertbutyloxycarbonyl.
53 <220> FEATURE:
54 <221> NAME/KEY: PEPTIDE
55 <222> LOCATION: (1)..(5)
56 <223> OTHER INFORMATION: OH signifies a free C-terminal carboxylic acid.
57 <220> FEATURE:
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60 <223> OTHER INFORMATION: A prefix "D" in D-Phe signifies that the
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64 1 5
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72 <221> NAME/KEY: PEPTIDE
73 <222> LOCATION: (1)..(5)
74 <223> OTHER INFORMATION: H signifies a free N-terminal amine.
75 <220> FEATURE:
76 <221> NAME/KEY: PEPTIDE
77 <222> LOCATION: (1)..(5)
78 <223> OTHER INFORMATION: OH signifies a free C-terminal carboxylic acid.
79 <220> FEATURE:
80 <221> NAME/KEY: PEPTIDE
81 <222> LOCATION: (1)..(5)
82 <223> OTHER INFORMATION: A prefix "D" in D-phe at position 4, signifies
83 that the phenylalanine is a D-amino acid.
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86 1 5
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93 <220> FEATURE:
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95 <222> LOCATION: (1)..(5)
96 <223> OTHER INFORMATION: Phe is a D-amino acid.
97 <400> SEQUENCE: 4
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99 1 5
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112 1 5
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121 <222> LOCATION: (1)..(6)
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124 Gly Arg Gly Asp Phe Val
125 1 5
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133 <221> NAME/KEY: PEPTIDE
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135 <223> OTHER INFORMATION: Val is a D-amino acid.
136 <400> SEQUENCE: 7
137 Arg Gly Asp Phe Val
138 1 5
139 <210> SEQ ID NO 8
140 <211> LENGTH: 15
141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide

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149 <211> LENGTH: 6
150 <212> TYPE: PRT
151 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
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154 <220> FEATURE:
155 <221> NAME/KEY: PEPTIDE
156 <222> LOCATION: (1)..(6)
157 <223> OTHER INFORMATION: N-methylated valine.
158 <220> FEATURE:
159 <221> NAME/KEY: PEPTIDE
160 <222> LOCATION: (1)..(6)
161 <223> OTHER INFORMATION: Phe is a D-amino acid.
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166 <211> LENGTH: 5
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168 <213> ORGANISM: Artificial Sequence
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172 <221> NAME/KEY: PEPTIDE
173 <222> LOCATION: (1)..(5)
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175 <220> FEATURE:
176 <221> NAME/KEY: PEPTIDE
177 <222> LOCATION: (5)..(5)
178 <223> OTHER INFORMATION: N-methylated valine
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181       1               5
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183 <211> LENGTH: 222
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 11
187   Lys Gly Ile Gln Glu Leu Tyr Gly Ala Ser Pro Asp Ile Asp Leu Gly
188       1               5               10               15
189   Thr Gly Pro Thr Pro Thr Leu Gly Pro Val Thr Pro Glu Ile Cys Lys
190           20           25           30
191   Gln Asp Ile Val Phe Asp Gly Ile Ala Gln Ile Arg Gly Glu Ile Phe
192       35           40           45
193   Phe Phe Lys Asp Arg Phe Ile Trp Arg Thr Val Thr Pro Arg Asp Lys
194       50           55           60

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195      Pro Met Gly Pro Leu Leu Val Ala Thr Phe Trp Pro Glu Leu Pro Glu
196      65                      70                      75                      80
197      Lys Ile Asp Ala Val Tyr Glu Ala Pro Gln Glu Glu Lys Ala Val Phe
198                      85                      90                      95
199      Phe Ala Gly Asn Glu Tyr Trp Ile Tyr Ser Ala Ser Thr Leu Glu Arg
200                      100                      105                      110
201      Gly Tyr Pro Lys Pro Leu Thr Ser Leu Gly Leu Pro Pro Asp Val Gln
202                      115                      120                      125
203      Arg Val Asp Ala Ala Phe Asn Trp Ser Lys Asn Lys Lys Thr Tyr Ile
204                      130                      135                      140
205      Phe Ala Gly Asp Lys Phe Trp Arg Tyr Asn Glu Val Lys Lys Lys Met
206      145                      150                      155                      160
207      Asp Pro Gly Phe Pro Lys Leu Ile Ala Asp Ala Trp Asn Ala Ile Pro
208                      165                      170                      175
209      Asp Asn Leu Asp Ala Val Val Asp Leu Gln Gly Gly Gly His Ser Tyr
210                      180                      185                      190
211      Phe Phe Lys Gly Ala Tyr Tyr Leu Lys Leu Glu Asn Gln Ser Leu Lys
212                      195                      200                      205
213      Ser Val Lys Phe Gly Ser Ile Lys Ser Asp Trp Leu Gly Cys
214                      210                      215                      220
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216 <211> LENGTH: 193
217 <212> TYPE: PRT
218 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 12
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221      1                      5                      10                      15
222      Glu Ile Phe Phe Phe Lys Asp Arg Phe Ile Trp Arg Thr Val Thr Pro
223                      20                      25                      30
224      Arg Asp Lys Pro Met Gly Pro Leu Leu Val Ala Thr Phe Trp Pro Glu
225                      35                      40                      45
226      Leu Pro Glu Lys Ile Asp Ala Val Tyr Glu Ala Pro Gln Glu Glu Lys
227                      50                      55                      60
228      Ala Val Phe Phe Ala Gly Asn Glu Tyr Trp Ile Tyr Ser Ala Ser Thr
229      65                      70                      75                      80
230      Leu Glu Arg Gly Tyr Pro Lys Pro Leu Thr Ser Leu Gly Leu Pro Pro
231                      85                      90                      95
232      Asp Val Gln Arg Val Asp Ala Ala Phe Asn Trp Ser Lys Asn Lys Lys
233                      100                      105                      110
234      Thr Tyr Ile Phe Ala Gly Asp Lys Phe Trp Arg Tyr Asn Glu Val Lys
235                      115                      120                      125
236      Lys Lys Met Asp Pro Gly Phe Pro Lys Leu Ile Ala Asp Ala Trp Asn
237                      130                      135                      140
238      Ala Ile Pro Asp Asn Leu Asp Ala Val Val Asp Leu Gln Gly Gly Gly
239      145                      150                      155                      160
240      His Ser Tyr Phe Phe Lys Gly Ala Tyr Tyr Leu Lys Leu Glu Asn Gln
241                      165                      170                      175
242      Ser Leu Lys Ser Val Lys Phe Gly Ser Ile Lys Ser Asp Trp Leu Gly
243                      180                      185                      190
244      Cys

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
